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RAW SEQUENCE LISTING DATE: 08/27/2004
 PATENT APPLICATION: US/10/724,273 TIME: 11:48:30

Input Set : N:\Crf3\RULE60\10724273.raw
 Output Set: N:\CRF4\08272004\J724273.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Palese, Peter

6 O'Neill, Robert

8 (ii) TITLE OF INVENTION: IDENTIFICATION AND USE OF ANTIVIRAL

9 COMPOUNDS THAT INHIBIT INTERACTION OF HOST CELL PROTEINS
10 AND VIRAL PROTEINS REQUIRED FOR VIRAL REPLICATION

12 (iii) NUMBER OF SEQUENCES: 20

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Pennie & Edmonds

16 (B) STREET: 1155 Avenue of the Americas

17 (C) CITY: New York

18 (D) STATE: New York

19 (E) COUNTRY: USA

20 (F) ZIP: 10036-2711

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk

24 (B) COMPUTER: IBM PC compatible

25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/10/724,273

C--> 30 (B) FILING DATE: 24-Nov-2003

31 (C) CLASSIFICATION: 514

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: US/08/444,994

34 (B) FILING DATE: 19-MAY-1995

35 (viii) ATTORNEY/AGENT INFORMATION:

36 (A) NAME: Coruzzi, Laura A.

37 (B) REGISTRATION NUMBER: 30,742

38 (C) REFERENCE/DOCKET NUMBER: 6923-054

40 (ix) TELECOMMUNICATION INFORMATION:

41 (A) TELEPHONE: (212) 790-9090

42 (B) TELEFAX: (212) 869-9741/8864

43 (C) TELEX: 66141 PENNIE

46 (2) INFORMATION FOR SEQ ID NO: 1:

48 (i) SEQUENCE CHARACTERISTICS:

49 (A) LENGTH: 19 base pairs

50 (B) TYPE: nucleic acid

51 (C) STRANDEDNESS: single

52 (D) TOPOLOGY: linear

W--> 54 (ii) MOLECULE TYPE: DNA

59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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61 GCAAAGCAGG AGAAACCAC
63 (2) INFORMATION FOR SEQ ID NO: 2:
65     (i) SEQUENCE CHARACTERISTICS:
66         (A) LENGTH: 24 base pairs
67         (B) TYPE: nucleic acid
68         (C) STRANDEDNESS: single
69         (D) TOPOLOGY: linear
W--> 71     (ii) MOLECULE TYPE: DNA
76     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
78 GGGTCCATCT GATAGATATG AGAG
80 (2) INFORMATION FOR SEQ ID NO: 3:
82     (i) SEQUENCE CHARACTERISTICS:
83         (A) LENGTH: 48 base pairs
84         (B) TYPE: nucleic acid
85         (C) STRANDEDNESS: single
86         (D) TOPOLOGY: linear
W--> 88     (ii) MOLECULE TYPE: DNA
91     (ix) FEATURE:
92         (A) NAME/KEY: modified_base
93         (B) LOCATION: 36
94         (D) OTHER INFORMATION: /mod_base= i
96     (ix) FEATURE:
97         (A) NAME/KEY: modified_base
98         (B) LOCATION: 37
99         (D) OTHER INFORMATION: /mod_base= i
101     (ix) FEATURE:
102         (A) NAME/KEY: modified_base
103         (B) LOCATION: 41
104         (D) OTHER INFORMATION: /mod_base= i
106     (ix) FEATURE:
107         (A) NAME/KEY: modified_base
108         (B) LOCATION: 42
109         (D) OTHER INFORMATION: /mod_base= i
111     (ix) FEATURE:
112         (A) NAME/KEY: modified_base
113         (B) LOCATION: 46
114         (D) OTHER INFORMATION: /mod_base= i
116     (ix) FEATURE:
117         (A) NAME/KEY: modified_base
118         (B) LOCATION: 47
119         (D) OTHER INFORMATION: /mod_base= i
122     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
124 CUACUACUAC UAGGCCACGC GTCGACTACT ACGGGNNGG NNGGGNNG
126 (2) INFORMATION FOR SEQ ID NO: 4:
128     (i) SEQUENCE CHARACTERISTICS:
129         (A) LENGTH: 20 base pairs
130         (B) TYPE: nucleic acid
131         (C) STRANDEDNESS: single
132         (D) TOPOLOGY: linear

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W--> 134      (ii) MOLECULE TYPE: DNA
139      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
141 TCCTGATGTT GCTGTAGACG
143 (2) INFORMATION FOR SEQ ID NO: 5:
145      (i) SEQUENCE CHARACTERISTICS:
146          (A) LENGTH: 20 base pairs
147          (B) TYPE: nucleic acid
148          (C) STRANDEDNESS: single
149          (D) TOPOLOGY: linear
20
W--> 151      (ii) MOLECULE TYPE: DNA
156      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
158 GCACGACTAG TATGATTTCG
160 (2) INFORMATION FOR SEQ ID NO: 6:
162      (i) SEQUENCE CHARACTERISTICS:
163          (A) LENGTH: 8 amino acids
164          (B) TYPE: amino acid
165          (C) STRANDEDNESS:
166          (D) TOPOLOGY: unknown
20
168      (ii) MOLECULE TYPE: peptide
173      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
175      Thr Gly Ala Gly Ala Gly Leu Gly
176      1          5
178 (2) INFORMATION FOR SEQ ID NO: 7:
180      (i) SEQUENCE CHARACTERISTICS:
181          (A) LENGTH: 5 amino acids
182          (B) TYPE: amino acid
183          (C) STRANDEDNESS:
184          (D) TOPOLOGY: unknown
186      (ii) MOLECULE TYPE: peptide
191      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
193      Tyr Ser Ala Ala Lys
194      1          5
196 (2) INFORMATION FOR SEQ ID NO: 8:
198      (i) SEQUENCE CHARACTERISTICS:
199          (A) LENGTH: 27 base pairs
200          (B) TYPE: nucleic acid
201          (C) STRANDEDNESS: single
202          (D) TOPOLOGY: unknown
27
W--> 204      (ii) MOLECULE TYPE: DNA
207      (ix) FEATURE:
208          (A) NAME/KEY: CDS
209          (B) LOCATION: 1..27
212      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
214 GAC TGG CTG GAA TTC CCC ATG GCG TCC
215 Asp Trp Leu Glu Phe Pro Met Ala Ser
216 1          5
219 (2) INFORMATION FOR SEQ ID NO: 9:
221      (i) SEQUENCE CHARACTERISTICS:
222          (A) LENGTH: 9 amino acids

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223         (B) TYPE: amino acid
224         (D) TOPOLOGY: linear
226     (ii) MOLECULE TYPE: protein
228     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
230 Asp Trp Leu Glu Phe Pro Met Ala Ser
231 1           5
233 (2) INFORMATION FOR SEQ ID NO: 10:
235     (i) SEQUENCE CHARACTERISTICS:
236         (A) LENGTH: 2940 base pairs
237         (B) TYPE: nucleic acid
238         (C) STRANDEDNESS: unknown
239         (D) TOPOLOGY: unknown
241     (ii) MOLECULE TYPE: cDNA
244     (ix) FEATURE:
245         (A) NAME/KEY: CDS
246         (B) LOCATION: 47..1663
249     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
251 CTAAC TTCAG CGGTGGCACC GGGATCGGTT GCCTTGAGCC TGAAAT ATG ACC ACC      55
252                                     Met Thr Thr
253                                     1
255 CCA GGA AAA GAG AAC TTT CGC CTG AAA AGT TAC AAG AAC AAA TCT CTG      103
256 Pro Gly Lys Glu Asn Phe Arg Leu Lys Ser Tyr Lys Asn Lys Ser Leu
257 5           10           15
259 AAT CCC GAT GAG ATG CGC AGG AGG AGG GAG GAA GAA GGA CTG CAG TTA      151
260 Asn Pro Asp Glu Met Arg Arg Arg Arg Glu Glu Glu Gly Leu Gln Leu
261 20          25          30          35
263 CGA AAG CAG AAA AGA GAA GAG CAG TTA TTC AAG CGG AGA AAT GTT GCT      199
264 Arg Lys Gln Lys Arg Glu Glu Gln Leu Phe Lys Arg Arg Asn Val Ala
265 40          45          50
267 ACA GCA GAA GAA GAA ACA GAA GAA GAA GTT ATG TCA GAT GGA GGC TTT      247
268 Thr Ala Glu Glu Glu Thr Glu Glu Glu Val Met Ser Asp Gly Gly Phe
269 55          60          65
271 CAT GAG GCT CAG ATT AGT AAC ATG GAG ATG GCA CCA GGT GGT GTC ATC      295
272 His Glu Ala Gln Ile Ser Asn Met Glu Met Ala Pro Gly Gly Val Ile
273 70          75          80
275 ACT TCT GAC ATG ATT GAG ATG ATA TTT TCC AAA AGC CCA GAG CAA CAG      343
276 Thr Ser Asp Met Ile Glu Met Ile Phe Ser Lys Ser Pro Glu Gln Gln
277 85          90          95
279 CTT TCA GCA ACA CAG AAA TTC AGG AAG CTG CTT TCA AAA GAA CCT AAC      391
280 Leu Ser Ala Thr Gln Lys Phe Arg Lys Leu Leu Ser Lys Glu Pro Asn
281 100         105         110         115
283 CCT CCT ATT GAT GAA GTT ATC AGC ACA CCA GGA GTA GTG GCC AGG TTT      439
284 Pro Pro Ile Asp Glu Val Ile Ser Thr Pro Gly Val Val Ala Arg Phe
285 120         125         130
287 GTG GAG TTC CTC AAA CGA AAA GAG AAT TGT TCA CTG CAG TTT GAA TCA      487
288 Val Glu Phe Leu Lys Arg Lys Glu Asn Cys Ser Leu Gln Phe Glu Ser
289 135         140         145
291 GCT TGG GTA CTG ACA AAT ATT GCT TCA GGA AAT TCT CTT CAG ACC CGA      535
292 Ala Trp Val Leu Thr Asn Ile Ala Ser Gly Asn Ser Leu Gln Thr Arg

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293	150	155	160	
295	ATT GTG ATT CAG GCA AGA GCT GTG CCC ATC TTC ATA GAG TTG CTC AGC	583		
296	Ile Val Ile Gln Ala Arg Ala Val Pro Ile Phe Ile Glu Leu Leu Ser			
297	165 170 175			
299	TCA GAG TTT GAA GAT GTC CAG GAA CAG GCA GTC TGG GCT CTT GGC AAC	631		
300	Ser Glu Phe Glu Asp Val Gln Glu Gln Ala Val Trp Ala Leu Gly Asn			
301	180 185 190 195			
303	ATT GCT GGA GAT AGT ACC ATG TGC AGG GAC TAT GTC TTA GAC TGC AAT	679		
304	Ile Ala Gly Asp Ser Thr Met Cys Arg Asp Tyr Val Leu Asp Cys Asn			
305	200 205 210			
307	ATC CTT CCC CCT CTT TTG CAG TTA TTT TCA AAG CAA AAC CGC CTG ACC	727		
308	Ile Leu Pro Pro Leu Leu Gln Leu Phe Ser Lys Gln Asn Arg Leu Thr			
309	215 220 225			
311	ATG ACC CGG AAT GCA GTA TGG GCT TTG TCT AAT CTC TGT AGA GGG AAA	775		
312	Met Thr Arg Asn Ala Val Trp Ala Leu Ser Asn Leu Cys Arg Gly Lys			
313	230 235 240			
315	AGT CCA CCT CCA GAA TTT GCA AAG GTT TCT CCA TGT CTG AAT GTG CTT	823		
316	Ser Pro Pro Pro Glu Phe Ala Lys Val Ser Pro Cys Leu Asn Val Leu			
317	245 250 255			
319	TCC TGG TTG CTG TTT GTC AGT GAC ACT GAT GTA CTG GCT GAT GCC TGC	871		
320	Ser Trp Leu Leu Phe Val Ser Asp Thr Asp Val Leu Ala Asp Ala Cys			
321	260 265 270 275			
323	TGG GCC CTC TCA TAT CTA TCA GAT GGA CCC AAT GAT AAA ATT CAA GCG	919		
324	Trp Ala Leu Ser Tyr Leu Ser Asp Gly Pro Asn Asp Lys Ile Gln Ala			
325	280 285 290			
327	GTC ATC GAT GCG GGA GTA TGT AGG AGA CTT GTG GAA CTG CTG ATG CAT	967		
328	Val Ile Asp Ala Gly Val Cys Arg Arg Leu Val Glu Leu Leu Met His			
329	295 300 305			
331	AAT GAT TAT AAA GTG GTT TCT CCT GCT TTG CGA GCT GTG GGA AAC ATT	1015		
332	Asn Asp Tyr Lys Val Val Ser Pro Ala Leu Arg Ala Val Gly Asn Ile			
333	310 315 320			
335	GTC ACA GGG GAT GAT ATT CAG ACA CAG GTA ATT CTG AAT TGC TCA GCT	1063		
336	Val Thr Gly Asp Asp Ile Gln Thr Gln Val Ile Leu Asn Cys Ser Ala			
337	325 330 335			
339	CTG CAG AGT TTA TTG CAT TTG CTG AGT AGC CCA AAG GAA TCT ATC AAA	1111		
340	Leu Gln Ser Leu Leu His Leu Leu Ser Ser Pro Lys Glu Ser Ile Lys			
341	340 345 350 355			
343	AAG GAA GCA TGT TGG ACG ATA TCT AAT ATT ACA GCT GGA AAT AGG GCA	1159		
344	Lys Glu Ala Cys Trp Thr Ile Ser Asn Ile Thr Ala Gly Asn Arg Ala			
345	360 365 370			
347	CAG ATC CAG ACT GTG ATA GAT GCC AAC ATT TTC CCA GCC CTC ATT AGT	1207		
348	Gln Ile Gln Thr Val Ile Asp Ala Asn Ile Phe Pro Ala Leu Ile Ser			
349	375 380 385			
351	ATT TTA CAA ACT GCT GAA TTT CGG ACA AGA AAA GAA GCA GCT TGG GCC	1255		
352	Ile Leu Gln Thr Ala Glu Phe Arg Thr Arg Lys Glu Ala Ala Trp Ala			
353	390 395 400			
355	ATC ACA AAT GCA ACT TCT GGA GGA TCA GCT GAA CAG ATC AAG TAC CTA	1303		
356	Ile Thr Asn Ala Thr Ser Gly Gly Ser Ala Glu Gln Ile Lys Tyr Leu			
357	405 410 415			

VERIFICATION SUMMARYPATENT APPLICATION: **US/10/724,273**

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Input Set : **N:\Crf3\RULE60\10724273.raw**Output Set: **N:\CRF4\08272004\J724273.raw**

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:54 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:71 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=2
L:88 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:134 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4
L:151 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5
L:204 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:672 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13
L:693 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14
L:942 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=16
L:967 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=17
L:990 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=18
L:1019 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=19